COMPARATIVE STUDY OF *AEROMONAS* SPECIES ISOLATED FROM FRESHWATER FISH AND HUMAN CLINICAL SPECIMENS

Boglárka Sellyei [1], Zsuzsanna Varga [1], Petra Paulus[3], Melitta Papp[3], Csaba Székely [1]

CAR HAS Institute for Veterinary Medical Research, Budapest, Hungary
National Food Chain Safety Office, Veterinary Diagnostic Directorate Budapest, Hungary

Aeromonas species are oxidase- and catalase-positive, glucose-fermenting, facultative anaerobic, gram-negative, rod-shaped bacteria. They are autochthonous to aquatic environments worldwide and have long been recognized as occasional pathogens. These bacteria have a broad host spectrum, with both cold- and warm-blooded animals, including man. In fish, they cause haemorrhagic septicaemia, fin rot, soft tissue rot and furunculosis. In humans, the most common clinical manifestations of Aeromonads infection are diarrhoea, gastroenteritis. In addition, they have role in induction of primary and secondary septicaemia in immunocompromised persons, wound infections in healthy individuals, and number of less well described illnesses such as endocarditis, peritonitis, meningitis, and infection of the eyes (corneal ulcers), joints, and bones. The genus *Aeromonas* consists of 31 species and is classified historically two main groups: non-motile, psychrophilic species, best represented by *A. salmonicida*, which generally responsible for fish and reptiles infection and a large group of motile mesophilic aeromonads which are associated with both piscine and human diseases.

The literature data suggest that the vast majority (≥85%) of clinical isolates attributed to three mesophilic *Aeromonas* species (*A. hydrophila*, *A. caviae*, and *A. veronii*). Since the available data suggest that they are the most frequently motile species in the diseased fish as well, aim of our study was to carry out comparative studies on some *Aeromonas* strains isolated from human clinical specimens (stool) and freshwater fishes (catfish, pike, sturgeon, eel). The studied species were *A. hydrophila*, *A. caviae*, *A. veronii* and some closely related spp. (*A. media, A. sobria)*. The traditional identification of strains was verified with sequence-analysis. For the detection of the occurrence of different virulence genes (lateral flagella, DNase, nuclease, serine protease, lipases, and toxins) was carried out with PCR, of the antimicrobial sensitivity (ampicillin, chloramphenicol, florfenicol, gentamicin, enrofloxacin, erythromycin, oxytetracycline, furazolidone, cotrimoxazole, polymyxin B) was applied the disc diffusion technique and of the pathogenicity with in vivo assay was studied.

Although, the results have not been able to reveal significant differences between piscine and human isolates at the studied features, the occurrence of variety virulence genes proved to be typical of each species or closely related species. These differences also manifested during the pathogenicity assays. The strains were characterised by inherited ampicillin resistance and moderate variances in the antimicrobial sensitivity against chloramphenicol, enrofloxacin. All strains were characterised by inherited ampicillin resistance and moderate differences were detectable in their antimicrobial susceptibility to erythromycin, oxytetracycline, and cotrimoxazole. Since the majority of human infection related to the aquatic environments, the similarity of *Aeromonas* isolates from fishes and man is reasonable. However, further studies are needed to clearly define the role of each species in the different type of piscine and human diseases.

This project was supported by KTIA-AIK-12-1-2013-0017, the Hungarian Scientific Research Fund (OTKA K 100132 and OTKA PD 101091) and by the János Bolyai Research Scholarship of the Hungarian Academy of Science to B. Sellyei

Acknowledge: Thanks Katalin Glatz M.D., Ph.D., who pointed out the importance of piscine Aeromonas species for the public health. In addition, thanks Katalin Kristóf M.D., Ph.D. (Eötvös Loránd University, Department of Laboratory Medicine) and Gábor Kardos M.D., Ph.D. (University of Debrecen, Department of Medical Microbiology) for their great help to obtain the human samples.